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RAW SEQUENCE LISTING DATE: 11/13/2001
PATENT APPLICATION: US/09/940,673 TIME: 15:26:02

Input Set : N:\CrF3\RULE60\09940673.txt
Output Set: N:\CRF3\11132001\I940673.raw

SEQUENCE LISTING

ENTERED

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70	CTGCTAAAC CCGCGCGGCT TTTACATTAG GAGTGAGTGG GGGAGAGTCC TAGGATTTCT	120
72	AGTAAAAAGT GACAGCGCTT GGTGGACTTT GGGACCTTCG TGAAGTCTTC TGCTTGGAAAG	180
74	CTGAGACTTG CATGCC ATG GAA CAC CCC CTC TTT GGC TGC CTG CGC AGC	229
75	Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser	
76	1 5 10	
78	CCC CAC GCC ACA GCG CAA GGC TTG CAC CCC TTC TCG CAG TCT TCT CTG	277
79	Pro His Ala Thr Ala Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu	
80	15 20 25	
82	GCC CTC CAT GGA AGA TCT GAC CAC ATG TCC TAC CCC GAA CTC TCC ACA	325
83	Ala Leu His Gly Arg Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr	
84	30 35 40	
86	TCT TCC TCG TCT TGC ATA ATC GCG GGA TAC CCC AAT GAG GAG GGC ATG	373
87	Ser Ser Ser Cys Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met	
88	45 50 55	
90	TTT GCC AGC CAG CATCAC AGG GGG CAC CAC CAC CAC CAC CAC CAC CAC	421
91	Phe Ala Ser Gln His His Arg Gly His His His His His His His His	
92	60 65 70 75	
94	CAT CAC CAC CAC CAG CAG CAG CAC CAG GCT CTG CAA AGC AAC TGG	469
95	His His His Gln Gln Gln His Gln Ala Leu Gln Ser Asn Trp	
96	80 85 90	
98	CAC CTC CCG CAG ATG TCC TCC CCG CCA AGC GCG GCC CGG CAC AGC CTT	517
99	His Leu Pro Gln Met Ser Ser Pro Pro Ser Ala Ala Arg His Ser Leu	
100	95 100 105	
102	TGC CTG CAG CCT GAT TCC GGA GGG CCC CCG GAG CTG GGG AGC AGC CCT	565
103	Cys Leu Gln Pro Asp Ser Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro	
104	110 115 120	
106	CCG GTC CTG TGC TCC AAC TCT TCT AGC CTG GGC TCC AGC ACC CCG ACC	613
107	Pro Val Leu Cys Ser Asn Ser Ser Leu Gly Ser Ser Thr Pro Thr	
108	125 130 135	
110	GGA GCC GCG TGC GCA CCA AGG GAT TAT GGC CGT CAA GCG CTG TCA CCC	661
111	Gly Ala Ala Cys Ala Pro Arg Asp Tyr Gly Arg Gln Ala Leu Ser Pro	
112	140 145 150 155	
114	GCA GAA GTG GAG AAG AGA AGT GGC AGC AAA AGA AAA AGC GAC AGT TCA	709
115	Ala Glu Val Glu Lys Arg Ser Gly Ser Lys Arg Lys Ser Asp Ser Ser	
116	160 165 170	
118	GAT TCC CAG GAA AAT TAC AAG TCA GAA GTG AAC AGC AAA CCT AGG	757
119	Asp Ser Gln Glu Gly Asn Tyr Lys Ser Glu Val Asn Ser Lys Pro Arg	
120	175 180 185	
122	AGG GAA AGA ACA GCT TTC ACC AAA GAG CAA ATC AGA GAA CTT GAG GCA	805
123	Arg Glu Arg Thr Ala Phe Thr Lys Glu Gln Ile Arg Glu Leu Glu Ala	
124	190 195 200	
126	GAG TTC GCC CAT CAT AAC TAT CTG ACC AGA CTG AGA AGA TAT GAG ATA	853
127	Glu Phe Ala His His Asn Tyr Leu Thr Arg Leu Arg Arg Tyr Glu Ile	
128	205 210 215	
130	GCG GTG AAC CTA GAC CTC ACT GAA AGA CAG GTG AAA GTG TGG TTC CAG	901
131	Ala Val Asn Leu Asp Leu Thr Glu Arg Gln Val Lys Val Trp Phe Gln	
132	220 225 230 235	
134	AAC AGG AGA ATG AAG TGG AAG CGG GTC AAG GGG GGA CAA CAA GGA GCT	949
135	Asn Arg Arg Met Lys Trp Lys Arg Val Lys Gly Gly Gln Gln Gly Ala	

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136	240	245	250	
138	GCA GCC CGA GAA AAG GAA CTG GTG AAT GTG AAA AAG GGA ACA CTT CTT			997
139	Ala Ala Arg Glu Lys Glu Leu Val Asn Val Lys Lys Gly Thr Leu Leu			
140	255	260	265	
142	CCA TCA GAG CTG TCA GGA ATT GGT GCA GCC ACC CTC CAG CAG ACA GGG			1045
143	Pro Ser Glu Leu Ser Gly Ile Gly Ala Ala Thr Leu Gln Gln Thr Gly			
144	270	275	280	
146	GAC TCA CTA GCA AAT GAC GAC AGT CGC GAT AGT GAC CAC AGC TCT GAG			1093
147	Asp Ser Leu Ala Asn Asp Asp Ser Arg Asp Ser Asp His Ser Ser Glu			
148	285	290	295	
150	CAC GCA CAC TTA TGATACATAC AGAGACCAGC TCCGTTCTCA GGAAAGCACC			1145
151	His Ala His Leu			
152	300			
154	ATTGTGATGG CAAATCTCAC CCAAACATCG TTTACATGGC AGATGACTGT GGCAGTGTG			1205
156	CTTAATATAA TTAAACGCAG GCATCTCAAG TCTGTTTCTC ATGATTGATA GAAGGTTTAC			1265
158	ACTAAGTGCC TCTTATTGAA GATGCTTCCA CAGTGAAATT GGAGAAAGTG AACATATCTA			1325
160	AATATACTTG TTCCTTATAT GACAGAGAGG GAGATGAATG TTTGCTTGG CTTGCACTGA			1385
162	AAATTAAATT GCTACCAAGA GCAAACCTCGG TAAGACATT TGACTCAAGT TGTCTCCAGA			1445
164	GTGAAGATGT TATAGAAATG CTTTGAACAT TCCAGTTGTA CCAGGTCACTG TGTGTGACAC			1505
166	TGGGCAGGTA TTTGCTTTG CTTGCACTGA AACTTAAACT GCTATCAAGT TAACCCATGA			1565
168	AATAGTTAT CTTGAACAGC CACAGTGCCT GAAATCACCA AGTGGATATA AAATGAAC			1625
170	AAATTCTGTA TATATTACTC CTAAGTCATT TTCCTGTCTT CACTAATTT AGCAAATGCA			1685
172	TTCATATTAG CTGATGAAAA TAGGCTTCC CGTGGACAAA TGCAGCCAGC TTCTTGTATT			1745
174	TTTATACATT TTTTGTCAAG TCAGAGACAT CAGTATGTGC TTACTTGTGT TCAAGTAGAG			1805
176	GAAATGCAGT AGAGTCTGAT AGGACATATT CTTGGTACCA CAGACAAAAC AAATCTTCTG			1865
178	TTGCATTGAC TATCAACTGC TCCAGATACA TTAGAGAAC CACCTAGCCC CCCTCCAGCC			1925
180	TCCCTCTGTT ATCGCTCGAA GACATTAGCG TCATAGGCAA GTAGTTACCT TGCCAAATGA			1985
182	GTCTTGTGTG GCAGATGTCT GATTTGTAT CTTTAAACTG TTAATGGTAT GTGTCTGCTT			2045
184	CAGTTAACAG GGAAAAAGAT TTCTTCCTCA TTGTTTATGA TACAAAACCC AAGTGCCAAA			2105
186	CAAAGCTAGT TCTTCAGGG ATAGATGAGA AACTGAATGT CTGACAAGTA GACTCAGCGA			2165
188	AAATACATTA TTTTCAGAG GCTGTGTATT CATGCAGTAC AAGTCCTTGT ATTTGTAAA			2225
190	AAAAAAAGTT AAATAAATG			2244

193 (2) INFORMATION FOR SEQ ID NO: 2:

195 (i) SEQUENCE CHARACTERISTICS:

- 196 (A) LENGTH: 303 amino acids
- 197 (B) TYPE: amino acid
- 198 (D) TOPOLOGY: linear

200 (ii) MOLECULE TYPE: protein

202 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

204	Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser Pro His Ala Thr Ala			
205	1	5	10	15
207	Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu Ala Leu His Gly Arg			
208	20	25	30	
210	Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr Ser Ser Ser Cys			
211	35	40	45	
213	Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met Phe Ala Ser Gln His			
214	50	55	60	
216	His Arg Gly His His His His His His His His His Gln			
217	65	70	75	80

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219 Gln Gln Gln His Gln Ala Leu Gln Ser Asn Trp His Leu Pro Gln Met
220 85 90 95
222 Ser Ser Pro Pro Ser Ala Ala Arg His Ser Leu Cys Leu Gln Pro Asp
223 100 105 110
225 Ser Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro Pro Val Leu Cys Ser
226 115 120 125
228 Asn Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr Gly Ala Ala Cys Ala
229 130 135 140
231 Pro Arg Asp Tyr Gly Arg Gln Ala Leu Ser Pro Ala Glu Val Glu Lys
232 145 150 155 160
234 Arg Ser Gly Ser Lys Arg Lys Ser Asp Ser Ser Asp Ser Gln Glu Gly
235 165 170 175
237 Asn Tyr Lys Ser Glu Val Asn Ser Lys Pro Arg Arg Glu Arg Thr Ala
238 180 185 190
240 Phe Thr Lys Glu Gln Ile Arg Glu Leu Glu Ala Glu Phe Ala His His
241 195 200 205
243 Asn Tyr Leu Thr Arg Leu Arg Arg Tyr Glu Ile Ala Val Asn Leu Asp
244 210 215 220
246 Leu Thr Glu Arg Gln Val Lys Val Trp Phe Gln Asn Arg Arg Met Lys
247 225 230 235 240
249 Trp Lys Arg Val Lys Gly Gly Gln Gln Gly Ala Ala Ala Arg Glu Lys
250 245 250 255
252 Glu Leu Val Asn Val Lys Lys Gly Thr Leu Leu Pro Ser Glu Leu Ser
253 260 265 270
255 Gly Ile Gly Ala Ala Thr Leu Gln Gln Thr Gly Asp Ser Leu Ala Asn
256 275 280 285
258 Asp Asp Ser Arg Asp Ser Asp His Ser Ser Glu His Ala His Leu
259 290 295 300

262 (2) INFORMATION FOR SEQ ID NO: 3:

264 (i) SEQUENCE CHARACTERISTICS:
265 (A) LENGTH: 941 base pairs
266 (B) TYPE: nucleic acid
267 (C) STRANDEDNESS: both
268 (D) TOPOLOGY: linear
270 (ii) MOLECULE TYPE: cDNA
272 (iii) HYPOTHETICAL: NO
274 (iv) ANTI-SENSE: NO
277 (ix) FEATURE:
278 (A) NAME/KEY: CDS
279 (B) LOCATION: 33..941
282 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

284 GTCTTCTACC TGGAAACCGA AACTTGCATG CT ATG GAA CAC CCG CTC TTT GGC	53
285 Met Glu His Pro Leu Phe Gly	
286 1 5	
288 TGC CTG CGC AGC CCT CAC GCC ACG GCG CAA GGC TTG CAC CCG TTC TCC	101
289 Cys Leu Arg Ser Pro His Ala Thr Ala Gln Gly Leu His Pro Phe Ser	
290 10 15 20	
292 CAA TCC TCT CTC GCC CTC CAT GGA AGA TCT GAC CAT ATG TCT TAC CCC	149
293 Gln Ser Ser Leu Ala Leu His Gly Arg Ser Asp His Met Ser Tyr Pro	

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294	25	30	35	
296	GAG CTC TCT ACT TCT TCC TCA TCT TGC ATA ATC GCG GGA TAC CCC AAC			197
297	Glu Leu Ser Thr Ser Ser Ser Cys Ile Ile Ala Gly Tyr Pro Asn			
298	40	45	50	55
300	GAA GAG GAC ATG TTT GCC AGC CAG CAT CAC AGG GGG CAC CAC CAC			245
301	Glu Glu Asp Met Phe Ala Ser Gln His His Arg Gly His His His			
302	60	65	70	
304	CAC CAC CAC CAT CAC CAC CAG CAG CAG CAG CAC CAG GCT CTG CAA			293
305	His His His His His His Gln Gln Gln His Gln Ala Leu Gln			
306	75	80	85	
308	ACC AAC TGG CAC CTC CCG CAG ATG TCT TCC CCA CCG AGT GCG GCT CGG			341
309	Thr Asn Trp His Leu Pro Gln Met Ser Ser Pro Pro Ser Ala Ala Arg			
310	90	95	100	
312	CAT AGC CTC TGC CTC CAG CCC GAC TCT GGA GGG CCC CCA GAG TTG GGG			389
313	His Ser Leu Cys Leu Gln Pro Asp Ser Gly Gly Pro Pro Glu Leu Gly			
314	105	110	115	
316	AGC AGC CCG CCC GTC CTG TGC TCC AAC TCT TCC AGC TTG GGC TCC AGC			437
317	Ser Ser Pro Pro Val Leu Cys Ser Asn Ser Ser Leu Gly Ser Ser			
318	120	125	130	135
320	ACC CCG ACT GGG GCC GCG TGC GCG CCG GGG GAC TAC GGC CGC CAG GCA			485
321	Thr Pro Thr Gly Ala Ala Cys Ala Pro Gly Asp Tyr Gly Arg Gln Ala			
322	140	145	150	
324	CTG TCA CCT GCG GAG GCG GAG AAG CGA AGC GGC GGC AAG AGG AAA AGC			533
325	Leu Ser Pro Ala Glu Ala Glu Lys Arg Ser Gly Gly Lys Arg Lys Ser			
326	155	160	165	
328	GAC AGC TCA GAC TCC CAG GAA GGA AAT TAC AAG TCA GAA GTC AAC AGC			581
329	Asp Ser Ser Asp Ser Gln Glu Gly Asn Tyr Lys Ser Glu Val Asn Ser			
330	170	175	180	
332	AAA CCC AGG AAA GAA AGG ACA GCA TTT ACC AAA GAG CAA ATC AGA GAA			629
333	Lys Pro Arg Lys Glu Arg Thr Ala Phe Thr Lys Glu Gln Ile Arg Glu			
334	185	190	195	
336	CTT GAA GCA GAA TTT GCC CAT CAT AAT TAT CTC ACC AGA CTG AGG CGA			677
337	Leu Glu Ala Glu Phe Ala His His Asn Tyr Leu Thr Arg Leu Arg Arg			
338	200	205	210	215
340	TAC GAG ATA GCA GTG AAT CTG GAT CTC ACT GAA AGA CAG GTA AAA GTC			725
341	Tyr Glu Ile Ala Val Asn Leu Asp Leu Thr Glu Arg Gln Val Lys Val			
342	220	225	230	
344	TGG TTC CAA AAC AGG CGG ATG AAG TGG AAG AGG GTA AAG GGT GGA CAG			773
345	Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Arg Val Lys Gly Gly Gln			
346	235	240	245	
348	CAA GGA GCT GCG GCT CGG GAA AAG GAA CTG GTG AAT GTG AAA AAG GGA			821
349	Gln Gly Ala Ala Ala Arg Glu Lys Glu Leu Val Asn Val Lys Lys Gly			
350	250	255	260	
352	ACA CTT CTC CCA TCA GAG CTG TCG GGA ATT GGT GCA GCC ACC CTC CAG			869
353	Thr Leu Leu Pro Ser Glu Leu Ser Gly Ile Gly Ala Ala Thr Leu Gln			
354	265	270	275	
356	CAA ACA GGG GAC TCT ATA GCA AAT GAA GAC AGT CAC GAC AGT GAC CAC			917
357	Gln Thr Gly Asp Ser Ile Ala Asn Glu Asp Ser His Asp Ser Asp His			
358	280	285	290	295

VERIFICATION SUMMARY
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TIME: 15:26:03

Input Set : N:\Crf3\RULE60\09940673.txt
Output Set: N:\CRF3\11132001\I940673.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]